



SEQUENCE LISTING

<110> COLLART, FRANK R.
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JOACIMIAK, ANDRZEJ
ZHANG, RONGGUANG
WESTBROOK, EDWIN M.

<120> USE OF CRYSTAL STRUCTURE OF BACTERIAL IMP DEHYDROGENASE
TO DESIGN INHIBITORS OF BACTERIAL GROWTH

<130> 21416/90042

<140> 09/533,466

<141> 2000-03-23

<160> 23

<170> PatentIn Ver. 2.1

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<211> 15

<212> PRT

<213> Streptococcus pyogenes

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<213> Bacillus subtilis

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<213> Escherichia coli

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 <213> *Mycobacterium tuberculosis*

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 <213> *Homo sapiens*

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 <213> *Leishmania donovani*

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 <213> *Saccharomyces cerevisiae*

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<213> *Drosophila melanogaster*

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<213> *Streptococcus pyogenes*

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<213> *Bacillus subtilis*

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Ala Asn Lys Leu Val Pro Glu Gly
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<213> *Bacillus subtilis*

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Phe Val Pro Glu Gly
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<212> PRT

<213> Mycobacterium tuberculosis

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<213> Homo sapiens

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Lys Ile Lys Val Ala Gln Gly
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<212> PRT

<213> Arabidopsis thaliana

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Lys Ile Ala Gln Gly
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 <223> "Xaa" represents selenomethionine

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      20              25              30

Leu Lys Thr Lys Leu Ala Asp Asn Leu Thr Leu Asn Ile Pro Ile Ile
      35              40              45

Thr Ala Ala Xaa Asp Thr Val Thr Gly Ser Lys Xaa Ala Ile Ala Ile
      50              55              60

Ala Arg Ala Gly Gly Leu Gly Val Ile His Lys Asn Xaa Ser Ile Thr
      65              70              75              80

Glu Gln Ala Glu Glu Val Arg Lys Val Lys Arg Ser Glu Asn Gly Val
      85              90              95

Ile Ile Asp Pro Phe Phe Leu Thr Pro Glu His Lys Val Ser Glu Ala
      100              105              110

Glu Glu Leu Xaa Gln Arg Tyr Arg Ile Ser Gly Val Pro Ile Val Glu
      115              120              125

Thr Leu Ala Asn Arg Lys Leu Val Gly Ile Ile Thr Asn Arg Asp Xaa
      130              135              140

Arg Phe Ile Ser Asp Tyr Asn Ala Pro Ile Ser Glu His Xaa Thr Ser
      145              150              155              160

Glu His Leu Val Thr Ala Ala Val Gly Thr Asp Leu Glu Thr Ala Glu
      165              170              175

Arg Ile Leu His Glu His Arg Ile Glu Lys Leu Pro Leu Val Asp Asn
      180              185              190

Ser Gly Arg Leu Ser Gly Leu Ile Thr Ile Lys Asp Ile Glu Lys Val
      195              200              205

Ile Glu Phe Pro His Ala Ala Lys Asp Glu Phe Gly Arg Leu Leu Val
      210              215              220

Ala Ala Ala Val Gly Val Thr Ser Asp Thr Phe Glu Arg Ala Glu Ala
      225              230              235              240

Leu Phe Glu Ala Gly Ala Asp Ala Ile Val Ile Asp Thr Ala His Gly
      245              250              255

His Ser Ala Gly Val Leu Arg Lys Ile Ala Glu Ile Arg Ala His Phe
      260              265              270

Pro Asn Arg Thr Leu Ile Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala
      275              280              285

Arg Ala Leu Tyr Asp Ala Gly Val Asp Val Val Lys Val Gly Ile Gly
      290              295              300

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Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val Gly Val Pro
 305 310 315 320
 Gln Val Thr Ala Ile Tyr Asp Ala Ala Ala Val Ala Arg Glu Tyr Gly
 325 330 335
 Lys Thr Ile Ile Ala Asp Gly Gly Ile Lys Tyr Ser Gly Asp Ile Val
 340 345 350
 Lys Ala Leu Ala Ala Gly Gly Asn Ala Val Xaa Leu Gly Ser Xaa Phe
 355 360 365
 Ala Gly Thr Asp Glu Ala Pro Gly Glu Thr Glu Ile Tyr Gln Gly Arg
 370 375 380
 Lys Tyr Lys Thr Tyr Arg Gly Xaa Gly Ser Ile Ala Ala Xaa Lys Lys
 385 390 395 400
 Asn Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Ala Tyr Lys Gly
 405 410 415
 Ala Ala Ser Asp Ile Val Phe Gln Xaa Leu Gly Gly Ile Arg Ser Gly
 420 425 430
 Xaa Gly Tyr Val Gly Ala Gly Asp Ile Gln Glu Leu His Glu Asn Ala
 435 440 445
 Gln Phe Val Glu Xaa Ser Gly Ala Gly Leu Ile Glu Ser His Pro His
 450 455 460
 Asp Val Gln Ile Thr Asn Glu Ala Pro Asn Tyr Ser Val
 465 470 475